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AMENDMENTS TO THE SPECIFICATION

IN THE SPECIFICATION

Amend the paragraph beginning on page 5, line 34 and ending on page 6, line 4 as follows:

Figure 1. **Alignment of *Homo sapiens* MANF1 and MANF2 amino acid sequences (SEQ ID NOS: 13 and 2 respectively)**. The alignment was generated with ClustalX program. Identical amino acid residues are marked with asterisk; based on the physicochemical characteristics of the residues high similarity is marked with a double colon and similarity with a dot. Signal sequences are underlined. Secondary structure alpha helix motifs are conserved between MANF1 and MANF2 and are marked above the sequences. Also the eight conserved cysteines are marked (boxed).

Amend the paragraph on page 6, line 6 as follows:

Figure 2. **Alignment of *Homo sapiens* and *Mus musculus* MANF2 amino acid sequences (SEQ ID NOS: 2 and 4 respectively)**. For explanations of the symbols, see FIG. 1.

Amend the paragraph on page 6, line 9 as follows:

Figure 3. **Alignment of MANF amino acid sequences from selected organisms.** The sequences were acquired by running Blast searches at the National Center for Biotechnology Information's www-server

(http://www.ncbi.nlm.nih.gov). In some cases the sequence was assembled from the genomic sequence and in some cases by assembling overlapping expressed sequence tags.

Mus musculus - MANF1	SEQ ID NO: 14
Rattus norvegivus	SEQ ID NO: 15
Homo sapiens -MANF1	SEQ ID NO: 13 (residues 27-179)
Bos Taurus	SEQ ID NO: 16
Gallus gallus	SEQ ID NO: 17
Xenopus laevis	SEQ ID NO: 18
Fugu rubribes	SEQ ID NO: 19
Danio rerio	SEQ ID NO: 20
Homo sapiens -MANF2	SEQ ID NO: 2 (residues 37-187)
Mus musculus - MANF2	SEQ ID NO: 4 (residues 37-187)
Drosophila melanogaster	SEQ ID NO: 21
Canorhabditis elegans	SEQ ID NO: 22

Amend the paragraph on page 9, line 4 as follows:

Figure 15. **Human MANF2 protein (SEQ ID NO: 2) secretory signal cleavage site**. Recombinant MANF2 protein containing original signal sequence was produced in COS-7 cells. Purified protein was subjected to tryptic digest, and peptide fragments were analyzed by Q-TOF mass spectrometry. Analysis verified the signal sequence cleavage site between amino acids at position 26 and 27.

IN THE SEQUENCE LISTING

Please replace the Sequence Listing of record with the Substitute Sequence Listing enclosed herewith.